Amendments to the Claims

The status of the claims is as follows:

1. (Currently Amended) A ~~hybridization assay~~ genus-specific probe comprising a target binding region ~~from~~ at least 18 ~~to 35~~ bases in length that fully hybridizes to a target sequence present in target nucleic acid derived from *Cryptosporidium* organisms in a test sample under stringent conditions to form a probe:target hybrid stable for detection, said target sequence being selected from the group consisting of SEQ ID NO:1, SEQ ID NO:2, SEQ ID NO:3 and SEQ ID NO:4, wherein said probe does not comprise a base region in addition to said target binding region that is capable of stably binding to said target nucleic acid under said conditions, and wherein said probe does not hybridize to nucleic acid derived from a non-*Cryptosporidium* organism in said test sample to form a probe:non-target hybrid stable for detection under said conditions.

Claims 2-6 (Canceled)

7. (Previously Presented) The probe of claim 1, wherein said probe contains at least two base regions that hybridize to each other when said probe is not hybridized to said target sequence under said conditions.

8. (Previously Presented) The probe of claim 1, wherein said probe comprises at least one base region that does not stably hybridize to nucleic acid derived from *Cryptosporidium* organisms under said conditions.

9. Canceled

10. (Original) The probe of claim 1 further comprising a detectable label.

11. (Previously Presented) The probe of claim 7 further comprising a group of interacting labels.

12. (Original) The probe of claim 11, wherein said interacting labels include a luminescent label and a quencher label.

13. (Previously Presented) The probe of claim 1, wherein said target binding region includes at least one ribonucleotide modified to include a 2'-O-methyl substitution to the ribofuranosyl moiety.

14. (Previously Presented) The probe of claim 1, wherein a pseudo peptide backbone joins at least a portion of the bases of said target binding region.

15. (Previously Presented) The probe of claim 1, wherein said conditions comprise 50 mM succinic acid, 1% (w/v) LLS, 7.5 mM aldrithiol-2, 0.6 M LiCl, 115 mM LiOH, 10 mM EDTA, 10 mM EGTA, 1.5% (v/v) ethyl alcohol (absolute), pH to 4.7, and a test sample temperature of about 60°C.

16. (Currently Amended) The probe of claim 1, wherein the base sequence of said target binding region is ~~at least 80%~~ perfectly complementary to the base sequence of said target sequence.

17. Canceled

18. (Currently Amended) The probe of claim 1, wherein the base sequence of said probe is ~~fully~~ perfectly complementary to the base sequence of said target sequence.

19. (Currently Amended) A probe mix comprising said probe of claim 1 and a first helper oligonucleotide from at least 18 ~~to 35~~ bases in length ~~which~~ that fully hybridizes to a target sequence selected from the group consisting of SEQ ID NO:21, SEQ ID NO:23, SEQ ID NO:25 and SEQ ID NO:27 under said conditions.

20. Canceled

21. (Withdrawn) The probe mix of claim 19 further comprising a second helper oligonucleotide ~~having an at least 10 contiguous base region which is at least 80% complementary to an at least 10 contiguous base region present in a target sequence, wherein the~~ at least 18 bases in length that fully hybridizes to a target sequence ~~of said second helper oligonucleotide is~~ selected from the group consisting of SEQ ID NO:22, SEQ ID NO:24, SEQ ID NO:26 and SEQ ID NO:28.

22. Canceled

23. (Currently Amended) An amplification oligonucleotide for use in amplifying a nucleic acid sequence present in target nucleic acid derived from *Cryptosporidium* organisms, said amplification oligonucleotide comprising a target binding region from at least 18 ~~to 40~~ bases in length ~~which~~ that fully hybridizes to a target sequence selected from the group consisting of SEQ ID NO:48, SEQ ID NO:54, SEQ ID NO:60 and SEQ ID NO:66 under amplification conditions, wherein said amplification oligonucleotide does not comprise a base region in addition to said target binding region that is capable of stably binding to said target nucleic acid under said conditions, and wherein said amplification oligonucleotide optionally includes a 5' sequence that is recognized by an RNA polymerase or which enhances initiation or elongation by an RNA polymerase.

Claims 24-32 (Canceled)

33. (Previously Presented) The amplification oligonucleotide of claim 23, wherein said amplification oligonucleotide includes said 5' sequence.

34. (Previously Presented) The amplification oligonucleotide of claim 33, wherein said 5' sequence is a T7 promoter having the base sequence of SEQ ID NO:69.

35. (Previously Presented) The amplification oligonucleotide of claim 23, wherein said amplification oligonucleotide contains at least two base regions that hybridize to each other when said amplification oligonucleotide is not hybridized to said target sequence under said conditions.

36. (Previously Presented) The amplification oligonucleotide of claim 35 further comprising a group of interacting labels.

37. (Previously Presented) The amplification oligonucleotide of claim 36, wherein said interacting labels include a luminescent label and a quencher label.

Claims 38 and 39 (Canceled)

40. (Currently Amended) The amplification oligonucleotide of claim 23, wherein the base sequence of said target binding region is ~~fully~~ perfectly complementary to the base sequence of said target sequence.

41. (Currently Amended) A set of amplification oligonucleotides for use in amplifying a nucleic acid sequence present in target nucleic acid derived from *Cryptosporidium* organisms, said set of amplification oligonucleotides including first and second amplification oligonucleotides, wherein said first amplification oligonucleotide is said amplification

oligonucleotide of claim 23,~~ and~~ wherein said second amplification oligonucleotide comprises a target binding region ~~from~~ at least 18 ~~to 40~~ bases in length ~~which~~ that fully hybridizes to a target sequence selected from the group consisting of SEQ ID NO:45, SEQ ID NO:46, SEQ ID NO:51, SEQ ID NO:52, SEQ ID NO:57, SEQ ID NO:58, SEQ ID NO:63 and SEQ ID NO:64 under amplification conditions, wherein said second amplification oligonucleotide does not comprise a base region in addition to said target binding region that is capable of stably binding to said target nucleic acid under said conditions, and wherein said second amplification oligonucleotide optionally includes a 5' sequence that is recognized by an RNA polymerase or that enhances initiation or elongation by an RNA polymerase.

42. Canceled

43. (Previously Presented) The set of amplification oligonucleotides of claim 41, wherein said target sequence of said second amplification oligonucleotide is selected from the group consisting of SEQ ID NO:45, SEQ ID NO:51, SEQ ID NO:57 and SEQ ID NO:63.

44. Canceled

45. (Previously Presented) The set of amplification oligonucleotides of claim 41, wherein said target sequence of said second amplification oligonucleotide is selected from the group consisting of SEQ ID NO:46, SEQ ID NO:52, SEQ ID NO:58 and SEQ ID NO:64.

Claims 46-49 (Canceled)

50. (Previously Presented) A method for determining the presence of *Cryptosporidium* organisms in a test sample, said method comprising the steps of:

contacting said test sample with said probe of claim 1 under stringent conditions; and

determining whether a probe:target hybrid has formed as an indication of the presence of *Cryptosporidium* organisms in said test sample.

51. (Previously Presented) A method for determining the presence of *Cryptosporidium* organisms in a test sample, said method comprising the steps of:

contacting said test sample with said probe of claim 16 under stringent conditions; and

determining whether a probe:target hybrid has formed as an indication of the presence of *Cryptosporidium* organisms in said test sample.

52. Canceled

53. (Previously Presented) A method for determining the presence of *Cryptosporidium* organisms in a test sample, said method comprising the steps of:

contacting said test sample with said probe of claim 18 under stringent conditions; and

determining whether a probe:target hybrid has formed as an indication of the presence of *Cryptosporidium* organisms in said test sample.

54. (Previously Presented) A method for amplifying *Cryptosporidium* nucleic acid that may be present in a test sample, said method comprising the steps of:

contacting said test sample with said amplification oligonucleotide of claim 23 under amplification conditions; and

amplifying a target sequence present in target nucleic acid derived from *Cryptosporidium* organisms that may be present in said test sample.

Claims 55-60 (Canceled)

61. (Currently Amended) The method of claim 54 further comprising ~~the step of~~ providing to said test sample a ~~hybridization assay~~ genus-specific probe for use in determining whether said target sequence was amplified in said amplifying step.

62. (Currently Amended) The method of claim 61, wherein said probe comprises a target binding region ~~from~~ at least 18 ~~to 35~~ bases in length that fully hybridizes to said target sequence or the complement thereof under stringent conditions to form a probe:target hybrid stable for detection, said target sequence or the complement thereof being selected from the group consisting of SEQ ID NO:1, SEQ ID NO:2, SEQ ID NO:3 and SEQ ID NO:4, wherein said probe does not comprise a base region in addition to said target binding region that is capable of stably binding to nucleic acid derived from *Cryptosporidium* organisms under said conditions, and wherein said probe does not hybridize to nucleic acid derived from a non-*Cryptosporidium* organism in said test sample to form a probe:non-target hybrid stable for detection under said conditions.

Claims 63-72 (Canceled)

73. (Previously Presented) A method for amplifying *Cryptosporidium* nucleic acid that may be present in a test sample, said method comprising the steps of:

contacting said test sample with said amplification oligonucleotide of claim 40 under amplification conditions; and

amplifying a target sequence present in target nucleic acid derived from *Cryptosporidium* organisms that may be present in said test sample.

74. (Currently Amended) A kit comprising, in packaged combination, first and second oligonucleotides for use in determining the presence of *Cryptosporidium* organisms in a test

sample, each of said oligonucleotides comprising a target binding region at least 18 bases in length that fully ~~which~~ hybridizes to a target sequence present in target nucleic acid derived from *Cryptosporidium* organisms under hybridization conditions, ~~said target binding region of said first oligonucleotide being from 18 to 35 bases in length and said target binding region of said second oligonucleotide being from 18 to 40 bases in length,~~ wherein said target sequence of said first oligonucleotide is selected from the group consisting of SEQ ID NO:1, SEQ ID NO:2, SEQ ID NO:3 and SEQ ID NO:4, wherein said target sequence of said second oligonucleotide is selected from the group consisting of SEQ ID NO:48, SEQ ID NO:54, SEQ ID NO:60 and SEQ ID NO:66, wherein ~~neither of~~ said ~~first and second~~ oligonucleotides ~~comprises~~ do not comprise a base region in addition to said target binding region that is capable of stably binding to said target nucleic acid under said conditions, and wherein said second oligonucleotide optionally includes a 5' sequence that is recognized by an RNA polymerase or that enhances initiation or elongation by an RNA polymerase.

Claims 75-82 (Canceled)

83. (Currently Amended) The kit of claim 74 further comprising a third oligonucleotide, said third oligonucleotide comprising a target binding region ~~from~~ at least 18 ~~to 40~~ bases in length ~~which~~ that fully hybridizes to a target sequence present in target nucleic acid derived from *Cryptosporidium* organisms under hybridization conditions, said target sequence being selected from the group consisting of SEQ ID NO:45, SEQ ID NO:51, SEQ ID NO:57 and SEQ ID NO:63, wherein said third oligonucleotide does not comprise a base region in addition to said target binding region that is capable of stably binding to said target nucleic acid under said conditions, and wherein said third oligonucleotide optionally includes a 5' sequence that is recognized by an RNA polymerase or that enhances initiation or elongation by an RNA polymerase.

84. Canceled

85. (Currently Amended) The kit of claim 74 further comprising a third oligonucleotide, said third oligonucleotide comprising a target binding region ~~from~~ at least 18 ~~to 40~~ bases in length ~~which~~ that fully hybridizes to a target sequence present in target nucleic acid derived from *Cryptosporidium* organisms under hybridization conditions, said target sequence being selected from the group consisting of SEQ ID NO:46, SEQ ID NO:52, SEQ ID NO:58 and SEQ ID NO:64, wherein said third oligonucleotide does not comprise a base region in addition to said target binding region that is capable of stably binding to said target nucleic acid under said conditions, and wherein said third oligonucleotide optionally includes a 5' sequence that is recognized by an RNA polymerase or that enhances initiation or elongation by an RNA polymerase.

Claims 86 and 87 (Canceled)

88. (Currently Amended) A kit comprising, in packaged combination, first and second oligonucleotides for use in determining the presence of *Cryptosporidium* organisms in a test sample, each of said oligonucleotides comprising a target binding region ~~from~~ at least 18 ~~to 35~~ bases in length that fully hybridizes to a target sequence present in target nucleic acid derived from *Cryptosporidium* organisms under stringent conditions, wherein said target sequence of said first oligonucleotide is selected from the group consisting of SEQ ID NO:1, SEQ ID NO:2, SEQ ID NO:3 and SEQ ID NO:4, wherein said target sequence of said second oligonucleotide is selected from the group consisting of SEQ ID NO:21, SEQ ID NO:23, SEQ ID NO:25 and SEQ ID NO:27, wherein ~~neither of~~ said ~~first and second~~ oligonucleotides ~~comprises~~ do not comprise a base region in addition to said target binding region that is capable of stably binding to said target nucleic acid under said conditions, and wherein said first oligonucleotide does not hybridize to nucleic acid derived from a non-*Cryptosporidium* organism in said test sample to form a probe:non-target hybrid stable for detection under said conditions.

Claims 89-96 (Canceled)

97. (Currently Amended) A probe mix comprising said probe of claim 18 and a first helper oligonucleotide, wherein the base sequence of said first helper oligonucleotide is ~~fully~~ perfectly complementary to the base sequence of a target sequence selected from the group consisting of SEQ ID NO:21, SEQ ID NO:23, SEQ ID NO:25 and SEQ ID NO:27.

98. (Currently Amended) The probe mix of claim 97 further comprising a second helper oligonucleotide, wherein the base sequence of said second helper oligonucleotide is ~~fully~~ perfectly complementary to the base sequence of a target sequence selected from the group consisting of SEQ ID NO:22, SEQ ID NO:24, SEQ ID NO:26 and SEQ ID NO:28.

Claims 99-105 (Canceled)

106. (Currently Amended) A set of amplification oligonucleotides for use in amplifying a nucleic acid sequence present in target nucleic acid derived from *Cryptosporidium* organisms, said set of amplification oligonucleotides including first and second amplification oligonucleotides, wherein said first amplification oligonucleotide is said amplification oligonucleotide of claim 40, ~~and~~ wherein said second amplification oligonucleotide comprises a target binding region, wherein the base sequence of said target binding region is ~~fully~~ perfectly complementary to the base sequence of a target sequence selected from the group consisting of SEQ ID NO:45, SEQ ID NO:46, SEQ ID NO:51, SEQ ID NO:52, SEQ ID NO:57, SEQ ID NO:58, SEQ ID NO:63 and SEQ ID NO:64, wherein said target binding region of said second amplification oligonucleotide hybridizes to said target sequence under amplification conditions, wherein said second amplification oligonucleotide does not comprise a base region in addition to said target binding region that is capable of stably binding to said target nucleic acid under said conditions, and wherein said second amplification oligonucleotide optionally includes a 5' sequence that is recognized by an RNA polymerase or that enhances initiation or elongation by an RNA polymerase.

107. (Previously Presented) The set of amplification oligonucleotides of claim 106, wherein said target sequence of said second amplification oligonucleotide is selected from the group consisting of SEQ ID NO:45, SEQ ID NO:51, SEQ ID NO:57 and SEQ ID NO:63.

108. (Previously Presented) The set of amplification oligonucleotides of claim 106, wherein said target sequence of said second amplification oligonucleotide is selected from the group consisting of SEQ ID NO:46, SEQ ID NO:52, SEQ ID NO:58 and SEQ ID NO:64.

109. Canceled

110. (Currently Amended) The method of claim 54 further comprising a second amplification oligonucleotide, said second amplification oligonucleotide comprising a target binding region ~~from~~ at least 18 ~~to 40~~ bases in length that fully hybridizes to a target sequence selected from the group consisting of SEQ ID NO:45, SEQ ID NO:51, SEQ ID NO:57 and SEQ ID NO:63 under said conditions, wherein said second amplification oligonucleotide does not comprise a base region in addition to said target binding region that is capable of stably binding to said target nucleic acid under said conditions, and wherein said second amplification oligonucleotide optionally includes a 5' sequence that is recognized by an RNA polymerase or that enhances initiation or elongation by an RNA polymerase.

111. (Currently Amended) The method of claim 110 further comprising the step of determining the presence of amplicon in said test sample with a ~~hybridization assay~~ genus-specific probe, wherein said probe comprises a target binding region ~~from~~ at least 18 ~~to 35~~ bases in length that fully hybridizes to a target sequence present in said amplicon under stringent conditions to form a probe:target hybrid stable for detection, said target sequence being selected from the group consisting of SEQ ID NO:1, SEQ ID NO:2, SEQ ID NO:3 and SEQ ID NO:4, wherein said probe does not comprise a base region in addition to said target binding region that is capable of stably

binding to said amplicon under said conditions, and wherein said probe does not hybridize to nucleic acid derived from a non-*Cryptosporidium* organism in said test sample to form a probe:non-target hybrid stable for detection under said conditions.

112. (Currently Amended) The method of claim 54 further comprising a second amplification oligonucleotide, said second amplification oligonucleotide comprising a target binding region ~~from~~ at least 18 ~~to 40~~ bases in length that fully hybridizes to a target sequence selected from the group consisting of SEQ ID NO:46, SEQ ID NO:52, SEQ ID NO:58 and SEQ ID NO:64 under said conditions, wherein said second amplification oligonucleotide does not comprise a base region in addition to said target binding region that is capable of stably binding to said target nucleic acid under said conditions, and wherein said second amplification oligonucleotide optionally includes a 5' sequence that is recognized by an RNA polymerase or that enhances initiation or elongation by an RNA polymerase.

113. (Currently Amended) The method of claim 112 further comprising the step of determining the presence of amplicon in said test sample with a ~~hybridization assay~~ genus-specific probe, wherein said probe comprises a target binding region ~~from~~ at least 18 ~~to 35~~ bases in length that fully hybridizes to a target sequence present in said amplicon under stringent conditions to form a probe:target hybrid stable for detection, said target sequence being selected from the group consisting of SEQ ID NO:1, SEQ ID NO:2, SEQ ID NO:3 and SEQ ID NO:4, wherein said probe does not comprise a base region in addition to said target binding region that is capable of stably binding to said amplicon under said conditions, and wherein said probe does not hybridize to nucleic acid derived from a non-*Cryptosporidium* organism in said test sample to form a probe:non-target hybrid stable for detection under said conditions.

Claims 114-129 (Canceled)

130. (Currently Amended) The method of claim 73 further comprising the step of determining the presence of amplicon in said test sample with ~~an oligonucleotide~~ a genus-specific probe, wherein the base sequence of said probe is ~~fully~~ perfectly complementary to the base sequence of a target sequence present in said amplicon, said target sequence being selected from the group consisting of SEQ ID NO:1, SEQ ID NO:2, SEQ ID NO:3 and SEQ ID NO:4.

131. (Currently Amended) The method of claim 73 further comprising a second amplification oligonucleotide comprising a target binding region, wherein the base sequence of said target binding region is ~~fully~~ perfectly complementary to the base sequence of a target sequence present in target nucleic acid derived from *Cryptosporidium* organisms, said target sequence being selected from the group consisting of SEQ ID NO:45, SEQ ID NO:51, SEQ ID NO:57 and SEQ ID NO:63, wherein said target binding region hybridizes to said target sequence under said conditions, wherein said second amplification oligonucleotide does not comprise a base region in addition to said target binding region that is capable of stably binding to said target nucleic acid under said conditions, and wherein said second amplification oligonucleotide optionally includes a 5' sequence that is recognized by an RNA polymerase or that enhances initiation or elongation by an RNA polymerase.

132. (Currently Amended) The method of claim 131 further comprising the step of determining the presence of amplicon in said test sample with ~~an oligonucleotide~~ a genus-specific probe, wherein the base sequence of said probe is ~~fully~~ perfectly complementary to the base sequence of a target sequence present in said amplicon, said target sequence being selected from the group consisting of SEQ ID NO:1, SEQ ID NO:2, SEQ ID NO:3 and SEQ ID NO:4.

133. (Currently Amended) The method of claim 73 further comprising a second amplification oligonucleotide comprising a target binding region, wherein the base sequence of said target binding region is ~~fully~~ perfectly complementary to the base sequence of a target sequence

present in target nucleic acid derived from *Cryptosporidium* organisms, said target sequence being selected from the group consisting of SEQ ID NO:46, SEQ ID NO:52, SEQ ID NO:58 and SEQ ID NO:64, wherein said target binding region hybridizes to said target sequence under said conditions, wherein said second amplification oligonucleotide does not comprise a base region in addition to said target binding region that is capable of stably binding to said target nucleic acid under said conditions, and wherein said second amplification oligonucleotide optionally includes a 5' sequence that is recognized by an RNA polymerase or that enhances initiation or elongation by an RNA polymerase.

134. (Currently Amended) The method of claim 133 further comprising the step of determining the presence of amplicon in said test sample with ~~an oligonucleotide~~ a genus-specific probe, wherein the base sequence of said probe is ~~fully~~ perfectly complementary to the base sequence of a target sequence present in said amplicon, said target sequence being selected from the group consisting of SEQ ID NO:1, SEQ ID NO:2, SEQ ID NO:3 and SEQ ID NO:4.

135. Canceled

136. (Currently Amended) The kit of claim 74, wherein the base sequence of said target binding region of each said oligonucleotide is ~~fully~~ perfectly complementary to the base sequence of said target sequence of said oligonucleotide.

137. Canceled

138. (Currently Amended) The kit of claim 74, wherein the base sequence of each said oligonucleotide is ~~fully~~ perfectly complementary to the base sequence of said target sequence of said oligonucleotide.

139. Canceled

140. (Currently Amended) The kit of claim 83, wherein the base sequence of said target binding region of each said oligonucleotide is ~~fully~~ perfectly complementary to the base sequence of said target sequence of said oligonucleotide.

141. Canceled

142. (Currently Amended) The kit of claim 83, wherein the base sequence of each said oligonucleotide is ~~fully~~ perfectly complementary to the base sequence of said target sequence of said oligonucleotide.

143. Canceled

144. (Currently Amended) The kit of claim 85, wherein the base sequence of said target binding region of each said oligonucleotide is ~~fully~~ perfectly complementary to the base sequence of said target sequence of said oligonucleotide.

145. Canceled

146. (Currently Amended) The kit of claim 85, wherein the base sequence of each said oligonucleotide is ~~fully~~ perfectly complementary to the base sequence of said target sequence of said oligonucleotide.

147. Canceled

148. (Currently Amended) The kit of claim 88, wherein the base sequence of said target binding region of each said oligonucleotide is ~~fully~~ perfectly complementary to the base sequence of said target sequence of said oligonucleotide.

149. Canceled

150. (Currently Amended) The kit of claim 88, wherein the base sequence of each said oligonucleotide is ~~fully~~ perfectly complementary to the base sequence of said target sequence of said oligonucleotide.

151. (Currently Amended) The kit of claim 88 further comprising a third oligonucleotide ~~from~~ at least 18 ~~to 35~~ bases in length that fully hybridizes to a target sequence present in target nucleic acid derived from *Cryptosporidium* organisms under said conditions, said target sequence being is selected from the group consisting of SEQ ID NO:22, SEQ ID NO:24, SEQ ID NO:26 and SEQ ID NO:28, wherein said third oligonucleotide does not comprise a base region in addition to said target binding region that is capable of stably binding to said target nucleic acid under said conditions.

152. Canceled

153. (Currently Amended) The kit of claim 151, wherein the base sequence of said target binding region of each said oligonucleotide is ~~fully~~ perfectly complementary to the base sequence of said target sequence of said oligonucleotide.

154. Canceled

155. (Currently Amended) The kit of claim 151, wherein the base sequence of each said oligonucleotide is ~~fully~~ perfectly complementary to the base sequence of said target sequence of said oligonucleotide.